



Attachment to  
Exer No 30

<b>Form 1449 (Modified)</b>  <b>Information Disclosure Statement By Applicant</b>  (Use Several Sheets if Necessary)	Atty Docket No.	Application No.:
	MXGNP002X1	09/495,668
	Applicant:	
	Selifonov et al.	
Filing Date	Group	
February 1, 2000	1637	

### U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1						
	A2						
	A3						
	A4						
	A5						
	A6						
	A7						
	A8						

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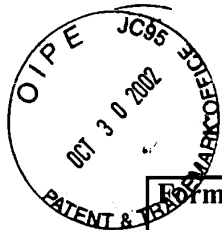
### Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1							
	B2							
	B3							
	B4							
	B5							

### Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Moore et al., <u>Modeling and Optimization of DNA Recombination</u> , Computer and Chemical Engineering 2000, Department of Chemical Engineering, The Pennsylvania State University, University Park © 2000
	C2	Gregory L. Moore, Costas D. Maranas, <u>Modeling DNA Mutation and Recombination for Directed Evolution Experiments</u> , Department of Chemical Engineering, The Pennsylvania State University, University Park, Received 28, October 1999, Accepted in revised form 15 April 2000 © 2000 Academic Press
Examiner	Date Considered 1-6-03	

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.



Attachment to Page No 2

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#### U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
<i>JA</i>	A1	6,125,331	9/26/00	Toh	—	—	
<i>JA</i>	A2	6,403,312	6/11/02	Dahiyat, et al	—	—	
<i>JA</i>	A3	6,455,254	9/24/02	Short	—	—	

#### Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
<i>JA</i>	B1	WO00/47612	8/17/00	WIPO	—	—		
<i>JA</i>	B2	WO01/61344	8/23/01	WIPO	—	—		
<i>JA</i>	B3	WO00/42559	7/2/00	WIPO	—	—		
<i>JA</i>	B4	WO01/75767	10/11/01	WIPO	—	—		

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#### Other Documents

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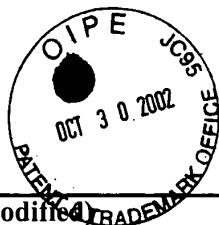
Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
<i>JA</i>	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," <i>Protein Science</i> 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," <i>Protein Science</i> , 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," <i>Protein Science</i> , 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," <i>Journal of Cellular Biochemistry Supplement</i> , 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," <i>Int. J. Peptide Protein Res.</i> 37:414-427 (1991)



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	C6	Martin van Heel, "A New Family of Powerful Multivariates Statistical Sequence Analysis Techniques," J. Mol. Biol, 220:877-887 (1991)
	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," Drug Dev. Research 33:125-132 (1994)
	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J. Mol. Recognit. 14:308-314 (2001)
	C9	Miyazawa et al., "Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading," J. Mol. Biol., 256:623-644 (1996)
	C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
	C11	Miyazawa et al., "Self-Consistent Estimation of Inter-Residue Protein Contact Energies Based on an Equilibrium Mixture Approximation of Residues," Proteins: Structure, Function, and Genetics, 34:49-68 (1999)
	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
	C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
	C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
	C16	H.W. Hellings, "Rational Protein Design: Combining Theory and Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
	C17	William F. DeGrado, "Proteins from Scratch," Science, Vol. 278, 80-81 (1997)



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	C18	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C19	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In <i>Escheruchua coli</i> Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C21	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
	C22	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)
	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994
Examiner		Date Considered 1-6-03

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